PT carbohydrates or enzymes.
XX
PS Claim 20; Page 244-245; 1246pp; English.
XX
CC AAF71360 to AAF71750 encode the Corynebacterium glutamicum sugar
CC metabolism and oxidative phosphorylation (SMP) proteins given in AAB79243
CC to AAB 79633 which are involved in carbon metabolism and energy
CC production. The C. glutamicum SMP gene can be used in vectors (II) for
CC expression in host cells and production or modulation of production of
CC fine chemicals, such as, an organic acid, a proteinogenic or
CC nonproteinogenic amino acid (preferred), a purine or pyrimidine base, a
CC nucleoside, a nucleotide, a lipid, a saturated or unsaturated fatty acid,
CC a diol, a carbohydrate, an aromatic compound, a vitamin, a cofactor, a
CC polyketide, or an enzyme. The presence of (I) or SMP proteins (III)
CC encoded by them are used for diagnosing the presence or activity of
CC Corynebacterium diphtheriae in a subject. (I), (II), (III) or host cells
CC containing them are used to map genomes of organisms related to C.
CC glutamicum, identify and localise C. glutamicum sequences of interest, in
CC evolutionary studies, in determining SMP protein regions required for
CC function, in modulating SMP protein activity, in modulating the
CC metabolism of sugars, and in modulating high-energy molecule production
CC in a cell (i.e. ATP, NADPH)
XX
SQ Sequence 425 AA;

Query Match 99.5%; Score 2145; DB 4; Length 425;
Best Local Similarity 99.5%; Pred. No. 8.1e-169;
Matches 423; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 VAEIMHVFAREILDSRGNPTVEAEVFLDDGSHGVAGVPSGASTGVHEAHELRDGGDRYLG 60
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Db          1 VAEIMHVFAREILDSRGNPTVEAEVFLDDGSHGVAGVPSGASTGVHEAHELRDGGDRYLG 60

Qy         61 KGVLKAVENVNEEIGDELAGLEADDQRLIDEAMIKLDGTANKSRLGANAILGVSMAVAKA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KGVLKAVENVNEEIGDELAGLEADDQRLIDEAMIKLDGTANKSRLGANAILGVSMAVAKA 120

Qy        121 AADSAGLPLFRYIGGPNAHVLPVPMMNIINGGAHADSGVDVQEFMIAPIGAETFSEALRN 180
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        121 AADSAGLPLFRYIGGPNAHVLPVPMMNIITGGAHADSGVDVQEFMIAPIGAETFSEALRN 180

Qy        181 GAEVYHALKSVIKEKGLSTGLGDEGGFAPSVGSTREALDLIVKAIEKAGFTPGKDIALAL 240
              ||||||||||||||||||||||||||||||||||||||||||||:||||||||||||||||
Db        181 GAEVYHALKSVIKEKGLSTGLGDEGGFAPSVGSTREALDLIVEAIEKAGFTPGKDIALAL 240

Qy        241 DVASSEFFKDGTYHFEGGQHSAAEMANVYAELVDAYPIVSIEDPLQEDDWEGYTNLTATI 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 DVASSEFFKDGTYHFEGGQHSAAEMANVYAELVDAYPIVSIEDPLQEDDWEGYTNLTATI 300

Qy        301 GDKVQIVGDDFFVTNPERLKEGIAKKAANSILVKVNQIGTLTETFDAVDMAHRAGYTSMM 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GDKVQIVGDDFFVTNPERLKEGIAKKAANSILVKVNQIGTLTETFDAVDMAHRAGYTSMM 360

Qy        361 SHRSGETEDTTIADLAVALNCGQIKTGAPARSDRVAKYNQLLRIEQLLGDAGVYAGRSAF 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 SHRSGETEDTTIADLAVALNCGQIKTGAPARSDRVAKYNQLLRIEQLLGDAGVYAGRSAF 420

Qy        421 PRFQG 425
              |||||
Db        421 PRFQG 425
```

RESULT 5
ADD13323
ID ADD13323 standard; protein; 425 AA.
XX
AC ADD13323;
XX
DT 01-JAN-2004 (first entry)
XX
DE C. glutamicum carbon metabolism associated protein RXA00235.
XX
KW carbon metabolism; energy-rich molecule; oxidative phosphorylation;
KW fine chemical; amino acid production; lysine production;
KW nucleotide production; nucleoside production; lipid production;
KW fatty acid production; diol production; carbohydrate production;
KW aromatic compound production; vitamin production; co-factor production;
KW enzyme production; food; animal feed; cosmetic; pharmaceutical.
XX
OS Corynebacterium glutamicum.
XX
FH Key Location/Qualifiers
FT Misc-difference 223
FT /note= "Optionally substituted with Lys"
XX
PN WO2003040291-A2.
XX
PD 15-MAY-2003.
XX
PF 31-OCT-2002; 2002WO-EP012135.
XX
PR 05-NOV-2001; 2001DE-01054270.
XX
PA (BADI) BASF AG.
XX
PI Zelder O, Pompejus M, Schroeder H, Kroeger B, Klopprogge C;
PI Haberhauer G;
XX
DR WPI; 2003-505068/47.
DR N-PSDB; ADD13322.
XX
PT New nucleic acid encoding variant forms of proteins involved in carbon
PT compound metabolism, useful for production of fine chemicals,
PT specifically lysine, in microorganisms.
XX
PS Claim 1; SEQ ID NO 8; 259pp; German.
XX
CC This invention describes novel polynucleotides and polypeptides
CC associated with the metabolism of carbon compounds and generation of
CC energy-rich molecules by oxidative phosphorylation in Corynebacterium
CC glutamicum. The polynucleotides of the invention are isolated from a
CC nucleic acid library of C. glutamicum then mutated at the specified
CC positions, cloned and expressed by standard methods. Cells, especially
CC Corynebacterium glutamicum, containing vectors that express the
CC polynucleotides are used for production of fine chemicals, preferably
CC amino acids and specifically lysine, but more generally nucleotides,
CC nucleosides, lipids, fatty acids, diols, carbohydrates, aromatic
CC compounds, vitamins, co-factors and enzymes. These are useful in the
CC food, animal feed, cosmetics and pharmaceutical industries.
CC Polynucleotides, optionally as primers and probes, can also be used for
CC identification and classification of C. glutamicum and related species,
CC e.g. for diagnosis; for genomic mapping; functional or evolutionary
CC studies gene manipulation, and modulation of metabolic activity. Cells
CC that contain the products of the invention may produce fine chemicals in
CC better yields, with higher productivity and/or more efficiently.
XX
SQ Sequence 425 AA;

Query Match 99.5%; Score 2145; DB 7; Length 425;
Best Local Similarity 99.5%; Pred. No. 8.1e-169;
Matches 423; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 VAEIMHVFAREILDSRGNPTVEAEVFLDDGSHGVAGVPSGASTGVHEAHELRDGGDRYLG 60
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Db          1 VAEIMHVFAREILDSRGNPTVEAEVFLDDGSHGVAGVPSGASTGVHEAHELRDGGDRYLG 60

Qy         61 KGVLKAVENVNEEIGDELAGLEADDQRLIDEAMIKLDGTANKSRLGANAILGVSMAVAKA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KGVLKAVENVNEEIGDELAGLEADDQRLIDEAMIKLDGTANKSRLGANAILGVSMAVAKA 120

Qy        121 AADSAGLPLFRYIGGPNAHVLPVPMMNIINGGAHADSGVDVQEFMIAPIGAETFSEALRN 180
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Db        121 AADSAGLPLFRYIGGPNAHVLPVPMMNIITGGAHADSGVDVQEFMIAPIGAETFSEALRN 180

Qy        181 GAEVYHALKSVIKEKGLSTGLGDEGGFAPSVGSTREALDLIVKAIEKAGFTPGKDIALAL 240
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XX
PN WO2003023016-A2.
XX
PD 20-MAR-2003.
XX
PF 11-SEP-2002; 2002WO-EP010174.
XX
PR 13-SEP-2001; 2001DE-01045043.
XX
PA (DEGS) DEGUSSA AG.
XX
PI Farwick M, Hermann T;
XX
DR WPI; 2003-354534/33.
DR N-PSDB; AGC45311.
XX
PT Microorganism useful for producing e.g. fine chemicals, has permanently
PT altered phosphorylatability protein, such that biosynthesis of fine
PT chemical synthesized by microorganism is increased compared to wild-type.
XX
PS Example 3; Page 80-81; 120pp; English.
XX
CC The present invention describes a microorganism (I), in which the
CC phosphorylatability of at least one protein has been permanently altered
CC such that the biosynthesis of at least one fine chemical synthesised by
CC the microorganism is increased compared to the wild type. Also described:
CC (1) use of a DNA (II) sequence coding for a protein which contains a
CC phosphorylation site, where the sequence contains such a mutation that
CC the protein is changed in its phosphorylatability for the production of
CC (I), or for the production of fine chemicals; and (2) a method for
CC producing fine chemicals or metabolites comprising using (I). (I) is
CC useful for producing fine chemicals or metabolites, such as amino acids,
CC vitamins, nucleosides, nucleotides, pigments or proteins. The amino acids
CC and vitamins produced using (I) can be used in human medicine, in the
CC pharmaceutical industry, food industry and in animal feeding. (I)
CC produces larger amount of desired fine chemical or a metabolite than the
CC wild type. The present sequence represents wild type eno from
CC Corynebacterium glutamicum, which is used in an example from the present
CC invention
XX
SQ Sequence 425 AA;

Query Match 99.7%; Score 2148; DB 6; Length 425;
Best Local Similarity 99.5%; Pred. No. 4.5e-169;
Matches 423; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 VAEIMHVFAREILDSRGNPTVEAEVFLDDGSHGVAGVPSGASTGVHEAHELRDGGDRYLG 60
              :||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAEIMHVFAREILDSRGNPTVEAEVFLDDGSHGVAGVPSGASTGVHEAHELRDGGDRYLG 60

Qy         61 KGVLKAVENVNEEIGDELAGLEADDQRLIDEAMIKLDGTANKSRLGANAILGVSMAVAKA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KGVLKAVENVNEEIGDELAGLEADDQRLIDEAMIKLDGTANKSRLGANAILGVSMAVAKA 120

Qy        121 AADSAGLPLFRYIGGPNAHVLPVPMMNIINGGAHADSGVDVQEFMIAPIGAETFSEALRN 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AADSAGLPLFRYIGGPNAHVLPVPMMNIINGGAHADSGVDVQEFMIAPIGAETFSEALRN 180

Qy        181 GAEVYHALKSVIKEKGLSTGLGDEGGFAPSVGSTREALDLIVEAIEKAGFTPGKDIALAL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAEVYHALKSVIKEKGLSTGLGDEGGFAPSVGSTREALDLIVEAIEKAGFTPGKDIALAL 240

Qy        241 DVASSEFFKDGTYHFEGGQHSAAEMANVYAELVDAYPIVSIEDPLQEDDWEGYTNLTATI 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 DVASSEFFKDGTYHFEGGQHSAAEMANVYAELVDAYPIVSIEDPLQEDDWEGYTNLTATI 300

Qy        301 GDKVQIVGDDFFVTNPERLKEGIAKKAANSILVKVNQIGTLTETFDAVDMAHRAGYTSMM 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GDKVQIVGDDFFVTNPERLKEGIAKKAANSILVKVNQIGTLTETFDAVDMAHRAGYTSMM 360

Qy        361 SHRSGETEDTTIADLAVALNCGQIKTGAPARSDRVAKYNQLLRIEQLLGDAGVYAGRSAF 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 SHRSGETEDTTIADLAVALNCGQIKTGAPARSDRVAKYNQLLRIEQLLGDAGVYAGRSAF 420
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Qy        421 PRFQG 425
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Db        421 PRFQG 425
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RESULT 4
AAB79278
ID AAB79278 standard; protein; 425 AA.
XX
AC AAB79278;
XX
DT 30-APR-2001 (first entry)
XX
DE Corynebacterium glutamicum SMP protein sequence SEQ ID NO:72.
XX
KW Corynebacterium glutamicum; carbon metabolism and energy production;
KW SMP protein; sugar metabolism and oxidative phosphorylation protein;
KW fine chemical production; organic acid; proteinogenic amino acid;
KW nonproteinogenic amino acid; purine base; pyrimidine base; nucleoside;
KW nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; diol;
KW carbohydrate; aromatic compound; vitamin; cofactor; polyketide; enzyme;
KW diagnosis; Corynebacterium diphtheriae; evolutionary study.
XX
OS Corynebacterium glutamicum.
XX
PN WO200100844-A2.
XX
PD 04-JAN-2001.
XX
PF 23-JUN-2000; 2000WO-IB000943.
XX
PR 25-JUN-1999; 99US-0141031P.
PR 08-JUL-1999; 99DE-01031412.
PR 08-JUL-1999; 99DE-01031413.
PR 08-JUL-1999; 99DE-01031419.
PR 08-JUL-1999; 99DE-01031420.
PR 08-JUL-1999; 99DE-01031424.
PR 08-JUL-1999; 99DE-01031428.
PR 08-JUL-1999; 99DE-01031431.
PR 08-JUL-1999; 99DE-01031433.
PR 08-JUL-1999; 99DE-01031434.
PR 08-JUL-1999; 99DE-01031510.
PR 08-JUL-1999; 99DE-01031562.
PR 08-JUL-1999; 99DE-01031634.
PR 09-JUL-1999; 99DE-01032180.
PR 09-JUL-1999; 99DE-01032227.
PR 09-JUL-1999; 99DE-01032230.
PR 09-JUL-1999; 99US-0143208P.
PR 14-JUL-1999; 99DE-01032924.
PR 14-JUL-1999; 99DE-01032973.
PR 14-JUL-1999; 99DE-01033005.
PR 27-AUG-1999; 99DE-01040765.
PR 31-AUG-1999; 99US-0151572P.
PR 03-SEP-1999; 99DE-01042076.
PR 03-SEP-1999; 99DE-01042079.
PR 03-SEP-1999; 99DE-01042086.
PR 03-SEP-1999; 99DE-01042087.
PR 03-SEP-1999; 99DE-01042088.
PR 03-SEP-1999; 99DE-01042095.
PR 03-SEP-1999; 99DE-01042123.
PR 03-SEP-1999; 99DE-01042125.
XX
PA (BADI) BASF AG.
XX
PI Pompejus M, Kroeger B, Schroeder H, Zelder O, Haberhauer G;
XX
DR WPI; 2001-061975/07.
DR N-PSDB; AAF71395.
XX
PT New isolated Corynebacterium glutamicum nucleic acid encoding a sugar
PT metabolism and oxidative phosphorylation protein for production or
PT modulation of production of fine chemicals e.g. amino acids,

BASF AKTIENGESELLSCHAFT (DE)

FEATURES Location/Qualifiers

source 1. .1398
/organism="Corynebacterium glutamicum"
/mol_type="unassigned DNA"
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CDS 101. .1378
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/db_xref="GI:12542658"
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ORIGIN

Query Match 88.4%; Score 1394.8; DB 6; Length 1398;
Best Local Similarity 99.9%; Pred. No. 1.9e-254;
Matches 1396; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy    51 CGAAACAAGATTCGTGCAACAATTGGGTGTAGACGTGATTGAAGACATTTGATCACGTGA 110
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Qy   111 ATAATTCTAGTTAGCTCCCAAGTTGGCATAGGAGGCCACAGTGGCTGAAATCATGCACGT 170
Db    61 ATAATTCTAGTTAGCTCCCAAGTTGGCATAGGAGGCCACAGTGGCTGAAATCATGCACGT 120

Qy   171 ATTCGCTCGCGAAATTCTCGACTCCCGCGGTAACCCAACCGTCGAGGCAGAGGTTTTCCT 230
Db   121 ATTCGCTCGCGAAATTCTCGACTCCCGCGGTAACCCAACCGTCGAGGCAGAGGTTTTCCT 180

Qy   231 GGATGACGGTTCCCACGGTGTCGCAGGTGTTCCATCCGGCGCATCCACCGGCGTCCACGA 290
Db   181 GGATGACGGTTCCCACGGTGTCGCAGGTGTTCCATCCGGCGCATCCACCGGCGTCCACGA 240

Qy   291 GGCTCATGAGCTGCGTGACGGTGGCGATCGCTACCTGGGCAAGGGCGTTTTGAAGGCAGT 350
Db   241 GGCTCATGAGCTGCGTGACGGTGGCGATCGCTACCTGGGCAAGGGCGTTTTGAAGGCAGT 300

Qy   351 TGAAAACGTCAACGAAGAAATCGGCGACGAGCTCGCTGGCCTAGAGGCTGACGATCAGCG 410
Db   301 TGAAAACGTCAACGAAGAAATCGGCGACGAGCTCGCTGGCCTAGAGGCTGACGATCAGCG 360

Qy   411 CCTCATCGACGAAGCAATGATCAAGCTTGATGGCACCGCCAACAAGTCCCGCCTGGGTGC 470
Db   361 CCTCATCGACGAAGCAATGATCAAGCTTGATGGCACCGCCAACAAGTCCCGCCTGGGTGC 420

Qy   471 AAACGCAATCCTTGGTGTTTCCATGGCTGTTGCAAAGGCTGCTGCTGATTCCGCAGGCCT 530
Db   421 AAACGCAATCCTTGGTGTTTCCATGGCTGTTGCAAAGGCTGCTGCTGATTCCGCAGGCCT 480

Qy   531 CCCACTGTTCCGCTACATCGGTGGACCAAACGCACACGTTCTTCCAGTTCCAATGATGAA 590
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Qy   591 CATCATCAACGGTGGCGCTCACGCTGACTCCGGTGTTGACGTTCAGGAATTCATGATCGC 650
Db   541 CATCATCACCGGTGGCGCTCACGCTGACTCCGGTGTTGACGTTCAGGAATTCATGATCGC 600

Qy   651 TCCAATCGGTGCAGAGACCTTCTCTGAGGCTCTCCGCAACGGCGCGGAGGTCTACCACGC 710
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Qy   711 ACTGAAGTCCGTCATCAAGGAAAAGGGCCTGTCCACCGGACTTGGCGATGAGGGCGGCTT 770
Db   661 ACTGAAGTCCGTCATCAAGGAAAAGGGCCTGTCCACCGGACTTGGCGATGAGGGCGGCTT 720

Qy   771 CGCTCCTTCCGTCGGCTCCACCCGTGAGGCTCTTGACCTTATCGTTAAGGCAATCGAGAA 830
Db   721 CGCTCCTTCCGTCGGCTCCACCCGTGAGGCTCTTGACCTTATCGTTGAGGCAATCGAGAA 780

Qy   831 GGCTGGCTTCACCCCAGGCAAGGACATCGCTCTTGCTCTGGACGTTGCTTCCTCTGAGTT 890
Db   781 GGCTGGCTTCACCCCAGGCAAGGACATCGCTCTTGCTCTGGACGTTGCTTCCTCTGAGTT 840

Qy   891 CTTCAAGGACGGCACCTACCACTTCGAAGGTGGCCAGCACTCCGCAGCTGAGATGGCAAA 950
Db   841 CTTCAAGGACGGCACCTACCACTTCGAAGGTGGCCAGCACTCCGCAGCTGAGATGGCAAA 900

Qy   951 CGTTTACGCTGAGCTCGTTGACGCGTACCCAATCGTCTCCATCGAGGACCCACTGCAGGA 1010
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Qy  1011 AGATGACTGGGAGGGTTACACCAACCTCACCGCAACCATCGGCGACAAGGTTCAGATCGT 1070
Db   961 AGATGACTGGGAGGGTTACACCAACCTCACCGCAACCATCGGCGACAAGGTTCAGATCGT 1020

Qy  1071 TGGCGACGACTTCTTCGTCACCAACCCTGAGCGCCTGAAGGAGGGCATCGCTAAGAAGGC 1130
Db  1021 TGGCGACGACTTCTTCGTCACCAACCCTGAGCGCCTGAAGGAGGGCATCGCTAAGAAGGC 1080

Qy  1131 TGCCAACTCCATCCTGGTTAAGGTGAACCAGATCGGTACCCTCACCGAGACCTTCGACGC 1190
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Qy  1191 TGTCGACATGGCTCACCGCGCAGGCTACACCTCCATGATGTCCCACCGTTCCGGTGAGAC 1250
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Qy  1251 CGAGGACACCACCATTGCTGACCTCGCAGTTGCACTCAACTGTGGCCAGATCAAGACTGG 1310
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Qy  1311 TGCTCCAGCACGTTCCGACCGTGTCGCAAAGTACAACCAGCTTCTCCGCATCGAGCAGCT 1370
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Qy  1371 GCTTGGCGACGCCGGCGTCTACGCAGGTCGCAGCGCATTCCCACGCTTTCAGGGCTAAAT 1430
Db  1321 GCTTGGCGACGCCGGCGTCTACGCAGGTCGCAGCGCATTCCCACGCTTTCAGGGCTAAAT 1380

Qy  1431 AAAAGCGCTTTTCGACGC 1448
Db  1381 AAAAGCGCTTTTCGACGC 1398
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RESULT 10
BD163286

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LOCUS       BD163286                1275 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Novel polynucleotide.
ACCESSION   BD163286
VERSION     BD163286.1  GI:27869050
KEYWORDS    JP 2002191370-A/1085.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 1275)
  AUTHORS   Nakagawa,S., Mizoguchi,H., Ando,S., Hayashi,M., Ochiai,K.,
            Yokoi,H., Tateishi,N., Senoo,A., Ikeda,M. and Ozaki,A.
  TITLE     Novel polynucleotide
  JOURNAL   Patent: JP 2002191370-A 1085 09-JUL-2002;
            KYOWA HAKKO KOGYO CO LTD
COMMENT     OS   Corynebacterium glutamicum
            PN   JP 2002191370-A/1085
            PD   09-JUL-2002
            PF   15-DEC-2000 JP 2000405096
            PI   SATOSHI NAKAGAWA,HIROSHI MIZOGUCHI,SEIKO ANDO,MIKIO HAYASHI,
            PI   KEIKO OCHIAI,
            PI   HARUHIKO YOKOI,NAOKO TATEISHI,AKIHIRO SENOO,MASATO IKEDA,AKIO
```

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          Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
          Corynebacterineae; Corynebacteriaceae; Corynebacterium.
REFERENCE 1
  AUTHORS   Zelder,O., Pompejus,M., Schroeder,H., Kroeger,B., Klopprogge,C. and
            Haberhauer,G.
  TITLE     Genes encoding for carbon metabolism and energy-producing proteins
  JOURNAL   Patent: WO 03040291-A 7 15-MAY-2003;
            BASF AKTIENGESELLSCHAFT (DE)
FEATURES             Location/Qualifiers
     source          1. .1405
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ORIGIN

  Query Match             88.8%;  Score 1401.8;  DB 6;  Length 1405;
  Best Local Similarity   99.9%;  Pred. No. 9.1e-256;
  Matches 1403;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

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Qy        111 ATAATTCTAGTTAGCTCCCAAGTTGGCATAGGAGGCCACAGTGGCTGAAATCATGCACGT 170
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Db         61 ATAATTCTAGTTAGCTCCCAAGTTGGCATAGGAGGCCACAGTGGCTGAAATCATGCACGT 120

Qy        171 ATTCGCTCGCGAAATTCTCGACTCCCGCGGTAACCCAACCGTCGAGGCAGAGGTTTTCCT 230
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ATTCGCTCGCGAAATTCTCGACTCCCGCGGTAACCCAACCGTCGAGGCAGAGGTTTTCCT 180

Qy        231 GGATGACGGTTCCCACGGTGTCGCAGGTGTTCCATCCGGCGCATCCACCGGCGTCCACGA 290
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GGATGACGGTTCCCACGGTGTCGCAGGTGTTCCATCCGGCGCATCCACCGGCGTCCACGA 240

Qy        291 GGCTCATGAGCTGCGTGACGGTGGCGATCGCTACCTGGGCAAGGGCGTTTTGAAGGCAGT 350
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GGCTCATGAGCTGCGTGACGGTGGCGATCGCTACCTGGGCAAGGGCGTTTTGAAGGCAGT 300

Qy        351 TGAAAACGTCAACGAAGAAATCGGCGACGAGCTCGCTGGCCTAGAGGCTGACGATCAGCG 410
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGAAAACGTCAACGAAGAAATCGGCGACGAGCTCGCTGGCCTAGAGGCTGACGATCAGCG 360

Qy        411 CCTCATCGACGAAGCAATGATCAAGCTTGATGGCACCGCCAACAAGTCCCGCCTGGGTGC 470
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CCTCATCGACGAAGCAATGATCAAGCTTGATGGCACCGCCAACAAGTCCCGCCTGGGTGC 420

Qy        471 AAACGCAATCCTTGGTGTTTCCATGGCTGTTGCAAAGGCTGCTGCTGATTCCGCAGGCCT 530
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AAACGCAATCCTTGGTGTTTCCATGGCTGTTGCAAAGGCTGCTGCTGATTCCGCAGGCCT 480

Qy        531 CCCACTGTTCCGCTACATCGGTGGACCAAACGCACACGTTCTTCCAGTTCCAATGATGAA 590
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CCCACTGTTCCGCTACATCGGTGGACCAAACGCACACGTTCTTCCAGTTCCAATGATGAA 540

Qy        591 CATCATCAACGGTGGCGCTCACGCTGACTCCGGTGTTGACGTTCAGGAATTCATGATCGC 650
               |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CATCATCACCGGTGGCGCTCACGCTGACTCCGGTGTTGACGTTCAGGAATTCATGATCGC 600
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Qy        651 TCCAATCGGTGCAGAGACCTTCTCTGAGGCTCTCCGCAACGGCGCGGAGGTCTACCACGC 710
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TCCAATCGGTGCAGAGACCTTCTCTGAGGCTCTCCGCAACGGCGCGGAGGTCTACCACGC 660

Qy        711 ACTGAAGTCCGTCATCAAGGAAAAGGGCCTGTCCACCGGACTTGGCGATGAGGGCGGCTT 770
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 ACTGAAGTCCGTCATCAAGGAAAAGGGCCTGTCCACCGGACTTGGCGATGAGGGCGGCTT 720

Qy        771 CGCTCCTTCCGTCGGCTCCACCCGTGAGGCTCTTGACCTTATCGTTAAGGCAATCGAGAA 830
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CGCTCCTTCCGTCGGCTCCACCCGTGAGGCTCTTGACCTTATCGTTGAGGCAATCGAGAA 780

Qy        831 GGCTGGCTTCACCCCAGGCAAGGACATCGCTCTTGCTCTGGACGTTGCTTCCTCTGAGTT 890
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GGCTGGCTTCACCCCAGGCAAGGACATCGCTCTTGCTCTGGACGTTGCTTCCTCTGAGTT 840

Qy        891 CTTCAAGGACGGCACCTACCACTTCGAAGGTGGCCAGCACTCCGCAGCTGAGATGGCAAA 950
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CTTCAAGGACGGCACCTACCACTTCGAAGGTGGCCAGCACTCCGCAGCTGAGATGGCAAA 900

Qy        951 CGTTTACGCTGAGCTCGTTGACGCGTACCCAATCGTCTCCATCGAGGACCCACTGCAGGA 1010
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CGTTTACGCTGAGCTCGTTGACGCGTACCCAATCGTCTCCATCGAGGACCCACTGCAGGA 960

Qy       1011 AGATGACTGGGAGGGTTACACCAACCTCACCGCAACCATCGGCGACAAGGTTCAGATCGT 1070
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AGATGACTGGGAGGGTTACACCAACCTCACCGCAACCATCGGCGACAAGGTTCAGATCGT 1020

Qy       1071 TGGCGACGACTTCTTCGTCACCAACCCTGAGCGCCTGAAGGAGGGCATCGCTAAGAAGGC 1130
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TGGCGACGACTTCTTCGTCACCAACCCTGAGCGCCTGAAGGAGGGCATCGCTAAGAAGGC 1080

Qy       1131 TGCCAACTCCATCCTGGTTAAGGTGAACCAGATCGGTACCCTCACCGAGACCTTCGACGC 1190
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TGCCAACTCCATCCTGGTTAAGGTGAACCAGATCGGTACCCTCACCGAGACCTTCGACGC 1140

Qy       1191 TGTCGACATGGCTCACCGCGCAGGCTACACCTCCATGATGTCCCACCGTTCCGGTGAGAC 1250
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TGTCGACATGGCTCACCGCGCAGGCTACACCTCCATGATGTCCCACCGTTCCGGTGAGAC 1200

Qy       1251 CGAGGACACCACCATTGCTGACCTCGCAGTTGCACTCAACTGTGGCCAGATCAAGACTGG 1310
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 CGAGGACACCACCATTGCTGACCTCGCAGTTGCACTCAACTGTGGCCAGATCAAGACTGG 1260

Qy       1311 TGCTCCAGCACGTTCCGACCGTGTCGCAAAGTACAACCAGCTTCTCCGCATCGAGCAGCT 1370
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 TGCTCCAGCACGTTCCGACCGTGTCGCAAAGTACAACCAGCTTCTCCGCATCGAGCAGCT 1320

Qy       1371 GCTTGGCGACGCCGGCGTCTACGCAGGTCGCAGCGCATTCCCACGCTTTCAGGGCTAAAT 1430
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 GCTTGGCGACGCCGGCGTCTACGCAGGTCGCAGCGCATTCCCACGCTTTCAGGGCTAAAT 1380

Qy       1431 AAAAGCGCTTTTCGACGCCCGGTAA 1455
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Db       1381 AAAAGCGCTTTTCGACGCCCGGTAA 1405
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RESULT 9
AX064945
LOCUS       AX064945               1398 bp    DNA     linear   PAT 24-JAN-2001
DEFINITION  Sequence 71 from Patent WO0100844.
ACCESSION   AX064945
VERSION     AX064945.1  GI:12542657
KEYWORDS    .
SOURCE      Corynebacterium glutamicum
  ORGANISM  Corynebacterium glutamicum
            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Corynebacterineae; Corynebacteriaceae; Corynebacterium.
REFERENCE   1
  AUTHORS   Pompejus,M., Kroeger,B., Schroeder,H., Zelder,O. and Haberhauer,G.
  TITLE     corynebacterium glutamicum genes encoding proteins involved in
            carbon metabolism and energy production
  JOURNAL   Patent: WO 0100844-A 71 04-JAN-2001;
```

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;  TITLE OF INVENTION:  PRODUCTION
;  FILE REFERENCE: BGI-126CPCN
;  CURRENT APPLICATION NUMBER: US/10/781,014
;  CURRENT FILING DATE:  2004-02-17
;  PRIOR APPLICATION NUMBER: US 09/602,740
;  PRIOR FILING DATE: 2000-06-23
;  PRIOR APPLICATION NUMBER: 60/141,031
;  PRIOR FILING DATE: 1999-06-25
;  PRIOR APPLICATION NUMBER: 60/143,208
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: 60/151,572
;  PRIOR FILING DATE: 1999-08-31
;  PRIOR APPLICATION NUMBER: DE 19931412.8
;  PRIOR FILING DATE: 1999-07-08
;  PRIOR APPLICATION NUMBER: DE 19931413.6
;  PRIOR FILING DATE: 1999-07-08
;  PRIOR APPLICATION NUMBER: DE 19931419.5
;  PRIOR FILING DATE: 1999-07-08
;  PRIOR APPLICATION NUMBER: DE 19931420.9
;  PRIOR FILING DATE: 1999-07-08
;  PRIOR APPLICATION NUMBER: DE 19931424.1
;  PRIOR FILING DATE: 1999-07-08
;  PRIOR APPLICATION NUMBER: DE 19931428.4
;  PRIOR FILING DATE: 1999-07-08
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 784
; SEQ ID NO 72
;   LENGTH: 425
;   TYPE: PRT
;   ORGANISM: Corynebacterium glutamicum
US-10-781-014-72

  Query Match             99.7%;  Score 2149;  DB 16;  Length 425;
  Best Local Similarity   99.8%;  Pred. No. 8.3e-171;
  Matches  424;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VAEIMHVFAREILDSRGNPTVEAEVFLDDGSHGVAGVPSGASTGVHEAHELRDGGDRYLG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VAEIMHVFAREILDSRGNPTVEAEVFLDDGSHGVAGVPSGASTGVHEAHELRDGGDRYLG 60

Qy         61 KGVLKAVENVNEEIGDELAGLEADDQRLIDEAMIKLDGTANKSRLGANAILGVSMAVAKA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KGVLKAVENVNEEIGDELAGLEADDQRLIDEAMIKLDGTANKSRLGANAILGVSMAVAKA 120

Qy        121 AADSAGLPLFRYIGGPNAHVLPVPMMNIINGGAHADSGVDVQEFMIAPIGAETFSEALRN 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AADSAGLPLFRYIGGPNAHVLPVPMMNIITGGAHADSGVDVQEFMIAPIGAETFSEALRN 180

Qy        181 GAEVYHALKSVIKEKGLSTGLGDEGGFAPSVGSTREALDLIVEAIEKAGFTPGKDIALAL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAEVYHALKSVIKEKGLSTGLGDEGGFAPSVGSTREALDLIVEAIEKAGFTPGKDIALAL 240

Qy        241 DVASSEFFKDGTYHFEGGQHSAAEMANVYAELVDAYPIVSIEDPLQEDDWEGYTNLTATI 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 DVASSEFFKDGTYHFEGGQHSAAEMANVYAELVDAYPIVSIEDPLQEDDWEGYTNLTATI 300

Qy        301 GDKVQIVGDDFFVTNPERLKEGIAKKAANSILVKVNQIGTLTETFDAVDMAHRAGYTSMM 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GDKVQIVGDDFFVTNPERLKEGIAKKAANSILVKVNQIGTLTETFDAVDMAHRAGYTSMM 360

Qy        361 SHRSGETEDTTIADLAVALNCGQIKTGAPARSDRVAKYNQLLRIEQLLGDAGVYAGRSAF 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 SHRSGETEDTTIADLAVALNCGQIKTGAPARSDRVAKYNQLLRIEQLLGDAGVYAGRSAF 420

Qy        421 PRFQG 425
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Db        421 PRFQG 425
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RESULT 7
US-10-494-836-8
; Sequence 8, Application US/10494836
; Publication No. US20050014233A1
; GENERAL INFORMATION:
;  APPLICANT: Zelder, Oskar
;  APPLICANT:  Pompejus, Markus
;  APPLICANT:  Schroder, Hartwig
;  APPLICANT:  Kroger, Burkhard
;  APPLICANT:  Klopprogge, Corinna
;  APPLICANT:  Haberhauer, Gregor
;  TITLE OF INVENTION: Genes coding for proteins of carbon metabolism and energy produc
;  FILE REFERENCE: BGI-167US
;  CURRENT APPLICATION NUMBER: US/10/494,836
;  CURRENT FILING DATE:  2004-05-05
;  PRIOR APPLICATION NUMBER: PCT/EP02/12135
;  PRIOR FILING DATE: 2002-10-31
;  PRIOR APPLICATION NUMBER: DE 101 54 270.4
;  PRIOR FILING DATE: 2001-11-05
;  NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 8
;   LENGTH: 425
;   TYPE: PRT
;   ORGANISM: Corynebacterium glutamicum
US-10-494-836-8

  Query Match             99.7%;  Score 2149;  DB 17;  Length 425;
  Best Local Similarity   99.8%;  Pred. No. 8.3e-171;
  Matches  424;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VAEIMHVFAREILDSRGNPTVEAEVFLDDGSHGVAGVPSGASTGVHEAHELRDGGDRYLG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VAEIMHVFAREILDSRGNPTVEAEVFLDDGSHGVAGVPSGASTGVHEAHELRDGGDRYLG 60

Qy         61 KGVLKAVENVNEEIGDELAGLEADDQRLIDEAMIKLDGTANKSRLGANAILGVSMAVAKA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KGVLKAVENVNEEIGDELAGLEADDQRLIDEAMIKLDGTANKSRLGANAILGVSMAVAKA 120

Qy        121 AADSAGLPLFRYIGGPNAHVLPVPMMNIINGGAHADSGVDVQEFMIAPIGAETFSEALRN 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AADSAGLPLFRYIGGPNAHVLPVPMMNIITGGAHADSGVDVQEFMIAPIGAETFSEALRN 180

Qy        181 GAEVYHALKSVIKEKGLSTGLGDEGGFAPSVGSTREALDLIVEAIEKAGFTPGKDIALAL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAEVYHALKSVIKEKGLSTGLGDEGGFAPSVGSTREALDLIVEAIEKAGFTPGKDIALAL 240

Qy        241 DVASSEFFKDGTYHFEGGQHSAAEMANVYAELVDAYPIVSIEDPLQEDDWEGYTNLTATI 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 DVASSEFFKDGTYHFEGGQHSAAEMANVYAELVDAYPIVSIEDPLQEDDWEGYTNLTATI 300

Qy        301 GDKVQIVGDDFFVTNPERLKEGIAKKAANSILVKVNQIGTLTETFDAVDMAHRAGYTSMM 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GDKVQIVGDDFFVTNPERLKEGIAKKAANSILVKVNQIGTLTETFDAVDMAHRAGYTSMM 360

Qy        361 SHRSGETEDTTIADLAVALNCGQIKTGAPARSDRVAKYNQLLRIEQLLGDAGVYAGRSAF 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 SHRSGETEDTTIADLAVALNCGQIKTGAPARSDRVAKYNQLLRIEQLLGDAGVYAGRSAF 420

Qy        421 PRFQG 425
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Db        421 PRFQG 425
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RESULT 8
US-10-282-122A-53908
; Sequence 53908, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, Liangsu
;  APPLICANT:  Zamudio, Carlos
;  APPLICANT:  Malone, Cheryl
;  APPLICANT:  Haselbeck, Robert
;  APPLICANT:  Ohlsen, Kari
;  APPLICANT:  Zyskind, Judith
;  APPLICANT:  Wall, Daniel
;  APPLICANT:  Trawick, John
;  APPLICANT:  Carr, Grant
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Db        301 GDKVQIVGDDFFVTNPERLKEGIAKKAANSILVKVNQIGTLTETFDAVDMAHRAGYTSMM 360

Qy        361 SHRSGETEDTTIADLAVALNCGQIKTGAPARSDRVAKYNQLLRIEQLLGDAGVYAGRSAF 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 SHRSGETEDTTIADLAVALNCGQIKTGAPARSDRVAKYNQLLRIEQLLGDAGVYAGRSAF 420

Qy        421 PRFQG 425
                |||||
Db        421 PRFQG 425


RESULT 4
US-09-860-768-4
; Sequence 4, Application US/09860768
; Patent No. US20020082403A1
; GENERAL INFORMATION:
;  APPLICANT: Mockel, Bettina
;  APPLICANT:  Pfefferle, Walter
;  APPLICANT:  Hermann, Thomas
;  APPLICANT:  Pohler, Alfred
;  APPLICANT:  Kalinowski, Jorn
;  APPLICANT:  Bathe, Brigitte
;  TITLE OF INVENTION: New Nucleotide Sequences that Code for the Eno Gene
;  FILE REFERENCE: 21123/278404
;  CURRENT APPLICATION NUMBER: US/09/860,768
;  CURRENT FILING DATE:  2001-05-21
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
;   LENGTH: 425
;   TYPE: PRT
;   ORGANISM: Corynebacterium glutamicum
US-09-860-768-4

  Query Match             99.8%;  Score 2151;  DB 9;  Length 425;
  Best Local Similarity   99.8%;  Pred. No. 5.6e-171;
  Matches  424;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VAEIMHVFAREILDSRGNPTVEAEVFLDDGSHGVAGVPSGASTGVHEAHELRDGGDRYLG 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VAEIMHVFAREILDSRGNPTVEAEVFLDDGSHGVAGVPSGASTGVHEAHELRDGGDRYLG 60

Qy         61 KGVLKAVENVNEEIGDELAGLEADDQRLIDEAMIKLDGTANKSRLGANAILGVSMAVAKA 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KGVLKAVENVNEEIGDELAGLEADDQRLIDEAMIKLDGTANKSRLGANAILGVSMAVAKA 120

Qy        121 AADSAGLPLFRYIGGPNAHVLPVPMMNIINGGAHADSGVDVQEFMIAPIGAETFSEALRN 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AADSAGLPLFRYIGGPNAHVLPVPMMNIINGGAHADSGVDVQEFMIAPIGAETFSEALRN 180

Qy        181 GAEVYHALKSVIKEKGLSTGLGDEGGFAPSVGSTREALDLIVEAIEKAGFTPGKDIALAL 240
                ||||||||||||||||||||||||||||||||||||||||||:|||||||||||||||||||
Db        181 GAEVYHALKSVIKEKGLSTGLGDEGGFAPSVGSTREALDLIVKAIEKAGFTPGKDIALAL 240

Qy        241 DVASSEFFKDGTYHFEGGQHSAAEMANVYAELVDAYPIVSIEDPLQEDDWEGYTNLTATI 300
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Db        241 DVASSEFFKDGTYHFEGGQHSAAEMANVYAELVDAYPIVSIEDPLQEDDWEGYTNLTATI 300

Qy        301 GDKVQIVGDDFFVTNPERLKEGIAKKAANSILVKVNQIGTLTETFDAVDMAHRAGYTSMM 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GDKVQIVGDDFFVTNPERLKEGIAKKAANSILVKVNQIGTLTETFDAVDMAHRAGYTSMM 360

Qy        361 SHRSGETEDTTIADLAVALNCGQIKTGAPARSDRVAKYNQLLRIEQLLGDAGVYAGRSAF 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 SHRSGETEDTTIADLAVALNCGQIKTGAPARSDRVAKYNQLLRIEQLLGDAGVYAGRSAF 420

Qy        421 PRFQG 425
                |||||
Db        421 PRFQG 425


RESULT 5
US-10-728-947-4
; Sequence 4, Application US/10728947
; Publication No. US20040220394A1
; GENERAL INFORMATION:
;  APPLICANT: Mockel, Bettina
;  APPLICANT:  Pfefferle, Walter
;  APPLICANT:  Hermann, Thomas
;  APPLICANT:  Pohler, Alfred
;  APPLICANT:  Kalinowski, Jorn
;  APPLICANT:  Bathe, Brigitte
;  TITLE OF INVENTION: New Nucleotide Sequences that Code for the Eno Gene
;  FILE REFERENCE: 21123/278404
;  CURRENT APPLICATION NUMBER: US/10/728,947
;  CURRENT FILING DATE:  2003-12-08
;  PRIOR APPLICATION NUMBER: US/09/860,768
;  PRIOR FILING DATE: 2001-05-21
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
;   LENGTH: 425
;   TYPE: PRT
;   ORGANISM: Corynebacterium glutamicum
US-10-728-947-4

  Query Match             99.8%;  Score 2151;  DB 16;  Length 425;
  Best Local Similarity   99.8%;  Pred. No. 5.6e-171;
  Matches  424;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VAEIMHVFAREILDSRGNPTVEAEVFLDDGSHGVAGVPSGASTGVHEAHELRDGGDRYLG 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VAEIMHVFAREILDSRGNPTVEAEVFLDDGSHGVAGVPSGASTGVHEAHELRDGGDRYLG 60

Qy         61 KGVLKAVENVNEEIGDELAGLEADDQRLIDEAMIKLDGTANKSRLGANAILGVSMAVAKA 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 KGVLKAVENVNEEIGDELAGLEADDQRLIDEAMIKLDGTANKSRLGANAILGVSMAVAKA 120

Qy        121 AADSAGLPLFRYIGGPNAHVLPVPMMNIINGGAHADSGVDVQEFMIAPIGAETFSEALRN 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AADSAGLPLFRYIGGPNAHVLPVPMMNIINGGAHADSGVDVQEFMIAPIGAETFSEALRN 180

Qy        181 GAEVYHALKSVIKEKGLSTGLGDEGGFAPSVGSTREALDLIVEAIEKAGFTPGKDIALAL 240
                ||||||||||||||||||||||||||||||||||||||||||:|||||||||||||||||||
Db        181 GAEVYHALKSVIKEKGLSTGLGDEGGFAPSVGSTREALDLIVKAIEKAGFTPGKDIALAL 240

Qy        241 DVASSEFFKDGTYHFEGGQHSAAEMANVYAELVDAYPIVSIEDPLQEDDWEGYTNLTATI 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 DVASSEFFKDGTYHFEGGQHSAAEMANVYAELVDAYPIVSIEDPLQEDDWEGYTNLTATI 300

Qy        301 GDKVQIVGDDFFVTNPERLKEGIAKKAANSILVKVNQIGTLTETFDAVDMAHRAGYTSMM 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GDKVQIVGDDFFVTNPERLKEGIAKKAANSILVKVNQIGTLTETFDAVDMAHRAGYTSMM 360

Qy        361 SHRSGETEDTTIADLAVALNCGQIKTGAPARSDRVAKYNQLLRIEQLLGDAGVYAGRSAF 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 SHRSGETEDTTIADLAVALNCGQIKTGAPARSDRVAKYNQLLRIEQLLGDAGVYAGRSAF 420

Qy        421 PRFQG 425
                |||||
Db        421 PRFQG 425


RESULT 6
US-10-781-014-72
; Sequence 72, Application US/10781014
; Publication No. US20040180408A1
; GENERAL INFORMATION:
;  APPLICANT: Pompejus, Markus
;  APPLICANT:  Kroger, Burkhard
;  APPLICANT:  Schroder, Hartwig
;  APPLICANT:  Zelder, Oskar
;  APPLICANT:  Haberhauer, Gregor
;  TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
;  TITLE OF INVENTION:  INVOLVED IN CARBON METABOLISM AND ENERGY
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Db        421 AAACGCAATCCTTGGTGTTTCCATGGCTGTTGCAAAGGCTGCTGCTGATTCCGCAGGCCT 480

Qy        531 CCCACTGTTCCGCTACATCGGTGGACCAAACGCACACGTTCTTCCAGTTCCAATGATGAA 590
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CCCACTGTTCCGCTACATCGGTGGACCAAACGCACACGTTCTTCCAGTTCCAATGATGAA 540

Qy        591 CATCATCAACGGTGGCGCTCACGCTGACTCCGGTGTTGACGTTCAGGAATTCATGATCGC 650
              |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CATCATCACCGGTGGCGCTCACGCTGACTCCGGTGTTGACGTTCAGGAATTCATGATCGC 600

Qy        651 TCCAATCGGTGCAGAGACCTTCTCTGAGGCTCTCCGCAACGGCGCGGAGGTCTACCACGC 710
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TCCAATCGGTGCAGAGACCTTCTCTGAGGCTCTCCGCAACGGCGCGGAGGTCTACCACGC 660

Qy        711 ACTGAAGTCCGTCATCAAGGAAAAGGGCCTGTCCACCGGACTTGGCGATGAGGGCGGCTT 770
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 ACTGAAGTCCGTCATCAAGGAAAAGGGCCTGTCCACCGGACTTGGCGATGAGGGCGGCTT 720

Qy        771 CGCTCCTTCCGTCGGCTCCACCCGTGAGGCTCTTGACCTTATCGTTGAGGCAATCGAGAA 830
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CGCTCCTTCCGTCGGCTCCACCCGTGAGGCTCTTGACCTTATCGTTGAGGCAATCGAGAA 780

Qy        831 GGCTGGCTTCACCCCAGGCAAGGACATCGCTCTTGCTCTGGACGTTGCTTCCTCTGAGTT 890
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GGCTGGCTTCACCCCAGGCAAGGACATCGCTCTTGCTCTGGACGTTGCTTCCTCTGAGTT 840

Qy        891 CTTCAAGGACGGCACCTACCACTTCGAAGGTGGCCAGCACTCCGCAGCTGAGATGGCAAA 950
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CTTCAAGGACGGCACCTACCACTTCGAAGGTGGCCAGCACTCCGCAGCTGAGATGGCAAA 900

Qy        951 CGTTTACGCTGAGCTCGTTGACGCGTACCCAATCGTCTCCATCGAGGACCCACTGCAGGA 1010
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CGTTTACGCTGAGCTCGTTGACGCGTACCCAATCGTCTCCATCGAGGACCCACTGCAGGA 960

Qy       1011 AGATGACTGGGAGGGTTACACCAACCTCACCGCAACCATCGGCGACAAGGTTCAGATCGT 1070
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AGATGACTGGGAGGGTTACACCAACCTCACCGCAACCATCGGCGACAAGGTTCAGATCGT 1020

Qy       1071 TGGCGACGACTTCTTCGTCACCAACCCTGAGCGCCTGAAGGAGGGCATCGCTAAGAAGGC 1130
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TGGCGACGACTTCTTCGTCACCAACCCTGAGCGCCTGAAGGAGGGCATCGCTAAGAAGGC 1080

Qy       1131 TGCCAACTCCATCCTGGTTAAGGTGAACCAGATCGGTACCCTCACCGAGACCTTCGACGC 1190
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TGCCAACTCCATCCTGGTTAAGGTGAACCAGATCGGTACCCTCACCGAGACCTTCGACGC 1140

Qy       1191 TGTCGACATGGCTCACCGCGCAGGCTACACCTCCATGATGTCCCACCGTTCCGGTGAGAC 1250
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TGTCGACATGGCTCACCGCGCAGGCTACACCTCCATGATGTCCCACCGTTCCGGTGAGAC 1200

Qy       1251 CGAGGACACCACCATTGCTGACCTCGCAGTTGCACTCAACTGTGGCCAGATCAAGACTGG 1310
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 CGAGGACACCACCATTGCTGACCTCGCAGTTGCACTCAACTGTGGCCAGATCAAGACTGG 1260

Qy       1311 TGCTCCAGCACGTTCCGACCGTGTCGCAAAGTACAACCAGCTTCTCCGCATCGAGCAGCT 1370
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 TGCTCCAGCACGTTCCGACCGTGTCGCAAAGTACAACCAGCTTCTCCGCATCGAGCAGCT 1320

Qy       1371 GCTTGGCGACGCCGGCGTCTACGCAGGTCGCAGCGCATTCCCACGCTTTCAGGGCTAAAT 1430
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 GCTTGGCGACGCCGGCGTCTACGCAGGTCGCAGCGCATTCCCACGCTTTCAGGGCTAAAT 1380

Qy       1431 AAAAGCGCTTTTCGACGC 1448
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Db       1381 AAAAGCGCTTTTCGACGC 1398
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RESULT 8
US-09-738-626-1085
; Sequence 1085, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAOKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 1085
; LENGTH: 1275
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-1085

Query Match 80.8%; Score 1275; DB 9; Length 1275;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1275; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        151 GTGGCTGAAATCATGCACGTATTCGCTCGCGAAATTCTCGACTCCCGCGGTAACCCAACC 210
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GTGGCTGAAATCATGCACGTATTCGCTCGCGAAATTCTCGACTCCCGCGGTAACCCAACC 60

Qy        211 GTCGAGGCAGAGGTTTTCCTGGATGAGGGTTCCCACGGTGTCGCAGGTGTTCCATCCGGC 270
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GTCGAGGCAGAGGTTTTCCTGGATGACGGTTCCCACGGTGTCGCAGGTGTTCCATCCGGC 120

Qy        271 GCATCCACCGGCGTCCACGAGGCTCATGAGCTGCGTGACGGTGGCGATCGCTACCTGGGC 330
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCATCCACCGGCGTCCACGAGGCTCATGAGCTGCGTGACGGTGGCGATCGCTACCTGGGC 180

Qy        331 AAGGGCGTTTTGAAGGCAGTTGAAAACGTCAACGAAGAAATCGGCGACGAGCTCGCTGGC 390
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AAGGGCGTTTTGAAGGCAGTTGAAAACGTCAACGAAGAAATCGGCGACGAGCTCGCTGGC 240

Qy        391 CTAGAGGCTGACGATCAGCGCCTCATCGACGAAGCAATGATCAAGCTTGATGGCACCGCC 450
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTAGAGGCTGACGATCAGCGCCTCATCGACGAAGCAATGATCAAGCTTGATGGCACCGCC 300

Qy        451 AACAAGTCCCGCCTGGGTGCAAACGCAATCCTTGGTGTTTCCATGGCTGTTGCAAAGGCT 510
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AACAAGTCCCGCCTGGGTGCAAACGCAATCCTTGGTGTTTCCATGGCTGTTGCAAAGGCT 360

Qy        511 GCTGCTGATTCCGCAGGCCTCCCACTGTTCCGCTACATCGGTGGACCAAACGCACACGTT 570
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCTGCTGATTCCGCAGGCCTCCCACTGTTCCGCTACATCGGTGGACCAAACGCACACGTT 420

Qy        571 CTTCCAGTTCCAATGATGAACATCATCAACGGTGGCGCTCACGCTGACTCCGGTGTTGAC 630
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CTTCCAGTTCCAATGATGAACATCATCAACGGTGGCGCTCACGCTGACTCCGGTGTTGAC 480

Qy        631 GTTCAGGAATTCATGATCGCTCCAATCGGTGCAGAGACCTTCTCTGAGGCTCTCCGCAAC 690
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTTCAGGAATTCATGATCGCTCCAATCGGTGCAGAGACCTTCTCTGAGGCTCTCCGCAAC 540

Qy        691 GGCGCGGAGGTCTACCACGCACTGAAGTCCGTCATCAAGGAAAAGGGCCTGTCCACCGGA 750
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GGCGCGGAGGTCTACCACGCACTGAAGTCCGTCATCAAGGAAAAGGGCCTGTCCACCGGA 600

Qy        751 CTTGGCGATGAGGGCGGCTTCGCTCCTTCCGTCGGCTCCACCCGTGAGGCTCTTGACCTT 810
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Qy        531 CCCACTGTTCCGCTACATCGGTGGACCAAACGCACACGTTCTTCCAGTTCCAATGATGAA 590
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CCCACTGTTCCGCTACATCGGTGGACCAAACGCACACGTTCTTCCAGTTCCAATGATGAA 540

Qy        591 CATCATCAACGGTGGCGCTCACGCTGACTCCGGTGTTGACGTTCAGGAATTCATGATCGC 650
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Db        541 CATCATCACCGGTGGCGCTCACGCTGACTCCGGTGTTGACGTTCAGGAATTCATGATCGC 600

Qy        651 TCCAATCGGTGCAGAGACCTTCTCTGAGGCTCTCCGCAACGGCGCGGAGGTCTACCACGC 710
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TCCAATCGGTGCAGAGACCTTCTCTGAGGCTCTCCGCAACGGCGCGGAGGTCTACCACGC 660

Qy        711 ACTGAAGTCCGTCATCAAGGAAAAGGGCCTGTCCACCGGACTTGGCGATGAGGGCGGCTT 770
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 ACTGAAGTCCGTCATCAAGGAAAAGGGCCTGTCCACCGGACTTGGCGATGAGGGCGGCTT 720

Qy        771 CGCTCCTTCCGTCGGCTCCACCCGTGAGGCTCTTGACCTTATCGTTGAGGCAATCGAGAA 830
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CGCTCCTTCCGTCGGCTCCACCCGTGAGGCTCTTGACCTTATCGTTGAGGCAATCGAGAA 780

Qy        831 GGCTGGCTTCACCCCAGGCAAGGACATCGCTCTTGCTCTGGACGTTGCTTCCTCTGAGTT 890
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GGCTGGCTTCACCCCAGGCAAGGACATCGCTCTTGCTCTGGACGTTGCTTCCTCTGAGTT 840

Qy        891 CTTCAAGGACGGCACCTACCACTTCGAAGGTGGCCAGCACTCCGCAGCTGAGATGGCAAA 950
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CTTCAAGGACGGCACCTACCACTTCGAAGGTGGCCAGCACTCCGCAGCTGAGATGGCAAA 900

Qy        951 CGTTTACGCTGAGCTCGTTGACGCGTACCCAATCGTCTCCATCGAGGACCCACTGCAGGA 1010
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CGTTTACGCTGAGCTCGTTGACGCGTACCCAATCGTCTCCATCGAGGACCCACTGCAGGA 960

Qy       1011 AGATGACTGGGAGGGTTACACCAACCTCACCGCAACCATCGGCGACAAGGTTCAGATCGT 1070
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AGATGACTGGGAGGGTTACACCAACCTCACCGCAACCATCGGCGACAAGGTTCAGATCGT 1020

Qy       1071 TGGCGACGACTTCTTCGTCACCAACCCTGAGCGCCTGAAGGAGGGCATCGCTAAGAAGGC 1130
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TGGCGACGACTTCTTCGTCACCAACCCTGAGCGCCTGAAGGAGGGCATCGCTAAGAAGGC 1080

Qy       1131 TGCCAACTCCATCCTGGTTAAGGTGAACCAGATCGGTACCCTCACCGAGACCTTCGACGC 1190
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TGCCAACTCCATCCTGGTTAAGGTGAACCAGATCGGTACCCTCACCGAGACCTTCGACGC 1140

Qy       1191 TGTCGACATGGCTCACCGCGCAGGCTACACCTCCATGATGTCCCACCGTTCCGGTGAGAC 1250
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TGTCGACATGGCTCACCGCGCAGGCTACACCTCCATGATGTCCCACCGTTCCGGTGAGAC 1200

Qy       1251 CGAGGACACCACCATTGCTGACCTCGCAGTTGCACTCAACTGTGGCCAGATCAAGACTGG 1310
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Db       1201 CGAGGACACCACCATTGCTGACCTCGCAGTTGCACTCAACTGTGGCCAGATCAAGACTGG 1260

Qy       1311 TGCTCCAGCACGTTCCGACCGTGTCGCAAAGTACAACCAGCTTCTCCGCATCGAGCAGCT 1370
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 TGCTCCAGCACGTTCCGACCGTGTCGCAAAGTACAACCAGCTTCTCCGCATCGAGCAGCT 1320

Qy       1371 GCTTGGCGACGCCGGCGTCTACGCAGGTCGCAGCGCATTCCCACGCTTTCAGGGCTAAAT 1430
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 GCTTGGCGACGCCGGCGTCTACGCAGGTCGCAGCGCATTCCCACGCTTTCAGGGCTAAAT 1380

Qy       1431 AAAAGCGCTTTTCGACGCCCGGTAA 1455
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Db       1381 AAAAGCGCTTTTCGACGCCCGGTAA 1405
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RESULT 7
US-10-781-014-71
; Sequence 71, Application US/10781014
; Publication No. US20040180408A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; TITLE OF INVENTION: INVOLVED IN CARBON METABOLISM AND ENERGY
; TITLE OF INVENTION: PRODUCTION
; FILE REFERENCE: BGI-126CPCN
; CURRENT APPLICATION NUMBER: US/10/781,014
; CURRENT FILING DATE: 2004-02-17
; PRIOR APPLICATION NUMBER: US 09/602,740
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/141,031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/143,208
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 60/151,572
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19931412.8
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931413.6
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931419.5
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931420.9
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931424.1
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931428.4
; PRIOR FILING DATE: 1999-07-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 784
; SEQ ID NO 71
; LENGTH: 1398
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (101)..(1375)
; OTHER INFORMATION: RXA00235
US-10-781-014-71

Query Match 88.5%; Score 1396.4; DB 19; Length 1398;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1397; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy         51 CGAAACAAGATTCGTGCAACAATTGGGTGTAGACGTGATTGAAGACATTTGATCACGTGA 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CGAAACAAGATTCGTGCAACAATTGGGTGTAGACGTGATTGAAGACATTTGATCACGTGA 60

Qy        111 ATAATTCTAGTTAGCTCCCAAGTTGGCATAGGAGGCCACAGTGGCTGAAATCATGCACGT 170
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATAATTCTAGTTAGCTCCCAAGTTGGCATAGGAGGCCACAGTGGCTGAAATCATGCACGT 120

Qy        171 ATTCGCTCGCGAAATTCTCGACTCCCGCGGTAACCCAACCGTCGAGGCAGAGGTTTTCCT 230
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ATTCGCTCGCGAAATTCTCGACTCCCGCGGTAACCCAACCGTCGAGGCAGAGGTTTTCCT 180

Qy        231 GGATGACGGTTCCCACGGTGTCGCAGGTGTTCCATCCGGCGCATCCACCGGCGTCCACGA 290
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GGATGACGGTTCCCACGGTGTCGCAGGTGTTCCATCCGGCGCATCCACCGGCGTCCACGA 240

Qy        291 GGCTCATGAGCTGCGTGACGGTGGCGATCGCTACCTGGGCAAGGGCGTTTTGAAGGCAGT 350
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GGCTCATGAGCTGCGTGACGGTGGCGATCGCTACCTGGGCAAGGGCGTTTTGAAGGCAGT 300

Qy        351 TGAAAACGTCAACGAAGAAATCGGCGACGAGCTCGCTGGCCTAGAGGCTGACGATCAGCG 410
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGAAAACGTCAACGAAGAAATCGGCGACGAGCTCGCTGGCCTAGAGGCTGACGATCAGCG 360

Qy        411 CCTCATCGACGAAGCAATGATCAAGCTTGATGGCACCGCCAACAAGTCCCGCCTGGGTGC 470
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CCTCATCGACGAAGCAATGATCAAGCTTGATGGCACCGCCAACAAGTCCCGCCTGGGTGC 420

Qy        471 AAACGCAATCCTTGGTGTTTCCATGGCTGTTGCAAAGGCTGCTGCTGATTCCGCAGGCCT 530
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